

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/170,042

DATE: 03/17/2000
TIME: 11:30:50

INPUT SET: S35072.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: HASTINGS, GREGG,
PATRICK J. DILLON

(ii) TITLE OF INVENTION: HUMAN NEURONAL ATTACHMENT FACTOR-1

(iii) NUMBER OF SEQUENCES: 18

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: HUMAN GENOME SCIENCES, INC.
(B) STREET: 9410 KEY WEST AVENUE
(C) CITY: ROCKVILLE
(D) STATE: MD
(E) COUNTRY: USA
(F) ZIP: 20850

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/170,042
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US/08/799,173
(B) FILING DATE: 11-FEB-1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: BROOKES, ANDERS A.
(B) REGISTRATION NUMBER: 36,373
(C) REFERENCE/DOCKET NUMBER: PF226

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (301) 309-8504
(B) TELEFAX: (301) 309-8512

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

RECEIVED
MAR 22 2000
TC 1000 MAIL ROOM
ENTERED

RAW SEQUENCE LISTING PATENT APPLICATION US/09/170,042

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47 (A) LENGTH: 1105 base pairs
 48 (B) TYPE: nucleic acid
 49 (C) STRANDEDNESS: single
 50 (D) TOPOLOGY: linear

51
52 (ii) MOLECULE TYPE: DNA (genomic)

53
54
55 (ix) FEATURE:

56 (A) NAME/KEY: CDS
 57 (B) LOCATION: 19..1011

58
59 (ix) FEATURE:

60 (A) NAME/KEY: mat_peptide
 61 (B) LOCATION: 19..963

62
63
64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

65	CGCTGCTCCT GCCGGGTG ATG GAA AAC CCC AGC CCG GCC GCC GCC CTG GGC	51
66	Met Glu Asn Pro Ser Pro Ala Ala Ala Leu Gly	
67	1 5 10	
68		
69	AAG GCC CTC TGC GCT CTC CTC CTG GCC ACT CTC GGC GCC GCC GGC CAG	99
70	Lys Ala Leu Cys Ala Leu Leu Leu Ala Thr Leu Gly Ala Ala Gly Gln	
71	15 20 25	
72		
73	CCT CTT GGG GGA GAG TCC ATC TGT TCC GCC AGA GCC CTG GCC AAA TAC	147
74	Pro Leu Gly Gly Glu Ser Ile Cys Ser Ala Arg Ala Leu Ala Lys Tyr	
75	30 35 40	
76		
77	AGC ATC ACC TTC ACG GGC AAG TGG AGC CAG ACG GCC TTC CCC AAG CAG	195
78	Ser Ile Thr Phe Thr Gly Lys Trp Ser Gln Thr Ala Phe Pro Lys Gln	
79	45 50 55	
80		
81	TAC CCC CTG TTC CGC CCC CCT GCC CAG TGG TCT TCG CTG CTG GGC GCC	243
82	Tyr Pro Leu Phe Arg Pro Pro Ala Gln Trp Ser Ser Leu Leu Gly Ala	
83	60 65 70 75	
84		
85	GCG CAT AGC TCC GAC TAC AGC ATG TGG AGG AAG AAC CAG TAC GTC AGT	291
86	Ala His Ser Ser Asp Tyr Ser Met Trp Arg Lys Asn Gln Tyr Val Ser	
87	80 85 90	
88		
89	AAC GGG CTG CGC GAC TTT GCG GAG CGC GGC GAG GCC TGG GCG CTG ATG	339
90	Asn Gly Leu Arg Asp Phe Ala Glu Arg Gly Glu Ala Trp Ala Leu Met	
91	95 100 105	
92		
93	AAG GAG ATC GAG GCG GCG GGG GAG GCG CTG CAG AGC GTG CAC GCG GTG	387
94	Lys Glu Ile Glu Ala Ala Gly Glu Ala Leu Gln Ser Val His Ala Val	
95	110 115 120	
96		
97	TTT TCG GCG CCC GCC GTC CCC AGC GGC ACC GGG CAG ACG TCG GCG GAG	435
98	Phe Ser Ala Pro Ala Val Pro Ser Gly Thr Gly Gln Thr Ser Ala Glu	
99		

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100	125	130	135	
101				483
102	CTG GAG GTG CAG CGC AGG CAC TCG CTG GTC TCG TTT GTG GTG CGC ATC			
103	Leu Glu Val Gln Arg Arg His Ser Leu Val Ser Phe Val Val Arg Ile			
104	140	145	150	155
105				531
106	GTG CCC AGC CCC GAC TGG TTC GTG GGC GTG GAC AGC CTG GAC CTG TGC			
107	Val Pro Ser Pro Asp Trp Phe Val Gly Val Asp Ser Leu Asp Leu Cys			
108		160	165	170
109				579
110	GAC GGG GAC CGT TGG CGG GAA CAG GCG GCG CTG GAC CTG TAC CCC TAC			
111	Asp Gly Asp Arg Trp Arg Glu Gln Ala Ala Leu Asp Leu Tyr Pro Tyr			
112		175	180	185
113				627
114	GAC GCC GGG ACG GAC AGC GGC TTC ACC TTC TCC TCC CCC AAC TTC GCC			
115	Asp Ala Gly Thr Asp Ser Gly Phe Thr Phe Ser Ser Pro Asn Phe Ala			
116		190	195	200
117				675
118	ACC ATC CCG CAG GAC ACG GTG ACC GAG ATA ACG TCC TCC TCT CCC AGC			
119	Thr Ile Pro Gln Asp Thr Val Thr Glu Ile Thr Ser Ser Ser Pro Ser			
120		205	210	215
121				723
122	CAC CCG GCC AAC TCC TTC TAC TAC CCG CGG CTG AAG GCC CTG CCT CCC			
123	His Pro Ala Asn Ser Phe Tyr Tyr Pro Arg Leu Lys Ala Leu Pro Pro			
124		220	225	230
125				235
126	ATC GCC AGG GTG ACA CTG GTG CGG CTG CGA CAG AGC CCC AGG GCC TTC			771
127	Ile Ala Arg Val Thr Leu Val Arg Leu Arg Gln Ser Pro Arg Ala Phe			
128		240	245	250
129				819
130	ATC CCT CCC GCC CCA GTC CTG CCC AGC AGG GAC AAT GAG ATT GTA GAC			
131	Ile Pro Pro Ala Pro Val Leu Pro Ser Arg Asp Asn Glu Ile Val Asp			
132		255	260	265
133				867
134	AGC GCC TCA GTT CCA GAA ACG CCG CTG GAC TGC GAG GTC TCC CTG TGG			
135	Ser Ala Ser Val Pro Glu Thr Pro Leu Asp Cys Glu Val Ser Leu Trp			
136		270	275	280
137				915
138	TCG TCC TGG GGA CTG TGC GGA GGC CAC TGT GGG AGG CTC GGG ACC AAG			
139	Ser Ser Trp Gly Leu Cys Gly Gly His Cys Gly Arg Leu Gly Thr Lys			
140		285	290	295
141				963
142	AGC AGG ACT CGC TAC GTC CGG GTC CAG CCC GCC AAC AAC GGG AGC CCC			
143	Ser Arg Thr Arg Tyr Val Arg Val Gln Pro Ala Asn Asn Gly Ser Pro			
144		300	305	310
145				315
146	TGC CCC GAG CTC GAA GAA GAG GCT GAG TGC GTC CCT GAT AAC TGC GTC			1011
147	Cys Pro Glu Leu Glu Glu Glu Ala Glu Cys Val Pro Asp Asn Cys Val			
148		320	325	330
149				1071
150	TAAGACCAGA GCGCCGACGC CCCTGGGGGCC CCGCGAGCC ATGGGGTGTC GGGGGCTCCT			
151				1105
152	GTGCAGGCTC ATGCTGCAGG CGGCCGAGGG CACA			

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153
154
155 (2) INFORMATION FOR SEQ ID NO:2:
156
157 (i) SEQUENCE CHARACTERISTICS:
158 (A) LENGTH: 331 amino acids
159 (B) TYPE: amino acid
160 (D) TOPOLOGY: linear
161
162 (ii) MOLECULE TYPE: protein
163
164 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
165
166 Met Glu Asn Pro Ser Pro Ala Ala Ala Leu Gly Lys Ala Leu Cys Ala
167 1 5 10 15
168
169 Leu Leu Leu Ala Thr Leu Gly Ala Ala Gly Gln Pro Leu Gly Gly Glu
170 20 25 30
171
172 Ser Ile Cys Ser Ala Arg Ala Leu Ala Lys Tyr Ser Ile Thr Phe Thr
173 35 40 45
174
175 Gly Lys Trp Ser Gln Thr Ala Phe Pro Lys Gln Tyr Pro Leu Phe Arg
176 50 55 60
177
178 Pro Pro Ala Gln Trp Ser Ser Leu Leu Gly Ala Ala His Ser Ser Asp
179 65 70 75 80
180
181 Tyr Ser Met Trp Arg Lys Asn Gln Tyr Val Ser Asn Gly Leu Arg Asp
182 85 90 95
183
184 Phe Ala Glu Arg Gly Glu Ala Trp Ala Leu Met Lys Glu Ile Glu Ala
185 100 105 110
186
187 Ala Gly Glu Ala Leu Gln Ser Val His Ala Val Phe Ser Ala Pro Ala
188 115 120 125
189
190 Val Pro Ser Gly Thr Gly Gln Thr Ser Ala Glu Leu Glu Val Gln Arg
191 130 135 140
192
193 Arg His Ser Leu Val Ser Phe Val Val Arg Ile Val Pro Ser Pro Asp
194 145 150 155 160
195
196 Trp Phe Val Gly Val Asp Ser Leu Asp Leu Cys Asp Gly Asp Arg Trp
197 165 170 175
198
199 Arg Glu Gln Ala Ala Leu Asp Leu Tyr Pro Tyr Asp Ala Gly Thr Asp
200 180 185 190
201
202 Ser Gly Phe Thr Phe Ser Ser Pro Asn Phe Ala Thr Ile Pro Gln Asp
203 195 200 205
204
205 Thr Val Thr Glu Ile Thr Ser Ser Ser Pro Ser His Pro Ala Asn Ser

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206 210 215 220
207
208 Phe Tyr Tyr Pro Arg Leu Lys Ala Leu Pro Pro Ile Ala Arg Val Thr
209 225 230 235 240
210
211 Leu Val Arg Leu Arg Gln Ser Pro Arg Ala Phe Ile Pro Pro Ala Pro
212 245 250 255
213
214 Val Leu Pro Ser Arg Asp Asn Glu Ile Val Asp Ser Ala Ser Val Pro
215 260 265 270
216
217 Glu Thr Pro Leu Asp Cys Glu Val Ser Leu Trp Ser Ser Trp Gly Leu
218 275 280 285
219
220 Cys Gly Gly His Cys Gly Arg Leu Gly Thr Lys Ser Arg Thr Arg Tyr
221 290 295 300
222
223 Val Arg Val Gln Pro Ala Asn Asn Gly Ser Pro Cys Pro Glu Leu Glu
224 305 310 315 320
225
226 Glu Glu Ala Glu Cys Val Pro Asp Asn Cys Val
227 325 330
228

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCCATACGGG ATCCCCAGCC TCTTGGGGGA GAGTCC

36

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

PAGE: 1

SEQUENCE VERIFICATION REPORT
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Original Text